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183492

From: Seharaseyon, Jegatheesan
Sent: Tuesday, March 28, 2006 4:06 PM
To: STIC-Biotech/ChemLib
Subject: Re:10/067832

Please search SEQ ID NO: 14 of 10/067832.

Thanks,

Seyon.

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Art Unit 1647
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STIC
MAR 28 2006
4:06 PM

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:01:25 ; Search time 79 Seconds
(without alignments)
183.538 Million cell updates/sec

Title: US-10-067-832D-14

Perfect score: 164

Sequence: 1 MIEVVCNDRLGKVKYKCNVTDITGDLKLLIAA 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	99.4	33	2	AAY08414 Human bea
2	163	99.4	33	8	ADR43346 Human Bea
3	163	99.4	73	2	AAY08413 P. obesu
4	163	99.4	73	3	AAB36290 Israeli s
5	163	99.4	73	4	AAM39680 Human pol
6	163	99.4	89	4	AAM41466 Human pol
7	163	99.4	115	5	ABP41331 Human ova
8	152	92.7	73	3	ABBS5910 Drosophil
9	147.5	89.9	32	3	AAB36291 Human bea
10	146	89.0	73	3	AAG40885 Zea mays
11	146	89.0	73	3	AAG41925 Arabidops
12	146	89.0	96	3	AAG41924 Arabidops
13	141	86.0	73	3	AAG27281 Zea mays
14	130.5	79.6	73	8	ADT58384 Plant pol
15	114	69.5	32	9	ADV95409 Yeast ubi
16	114	69.5	40	9	ADV95411 Yeast ubi
17	114	69.5	89	5	ADH32312 Novel yea
18	114	69.5	320	6	ABR83620 HUB1-GFP
19	68	41.5	27	4	AAM21187 Peptide #
20	68	41.5	27	4	ABM43508 Peptide #
21	68	41.5	27	4	AAM37402 Peptide #
22	68	41.5	27	4	ABB26468 Protein #
23	68	41.5	27	4	AAM77251 Human bon
24	68	41.5	27	4	AAM64443 Human bra

25	68	41.5	27	5	ABG46267 Human pep
26	56.5	34.5	282	2	AAR34706 NAD cycla
27	56.5	34.5	282	2	AAR70095 NAD cycla
28	56.5	34.5	282	2	Aaw80290 Aplysia c
29	54.5	33.2	169	8	ADX73119 Plant ful
30	54	32.9	525	6	ADA48272 Rice prot
31	54	32.9	525	7	ADC07784 Rice prot
32	53.5	32.6	1186	5	ABB93602 Herbicida
33	52.5	32.0	630	4	ABB61655 Drosophil
34	52.5	32.0	831	5	ABG91571 Purine/py
35	52	31.7	231	7	ADC95674 E. faeciu
36	52	31.7	1094	3	AAB23858 Haemophil
37	51	31.1	37	6	ABU61308 Human A d
38	51	31.1	37	8	ADP21530 Human LDL
39	51	31.1	527	7	ADE07959 Novel pro
40	51	31.1	527	8	ADO47164 Amino aci
41	51	31.1	527	8	ADP12444 Protein e
42	51	31.1	527	9	ADW47997 Recombina
43	51	31.1	3197	7	ABM85418 Mouse pro
44	51	31.1	4183	7	ABM85419 Human pro
45	51	31.1	4419	8	ADN11590 Human CDS

ALIGNMENTS

RESULT 1

AAY08414

ID AAY08414 standard; protein; 33 AA.

AC AAY08414;

DT 24-JUL-1999 (first entry)

DE Human beacon protein.

XX Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;

KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;

KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;

KW medicament; livestock; diagnosis; human.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /label= unknown

FT /note= "encoded by CNC"

XX WO9923217-A1.

XX

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XX

CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
 CC resistance. The beacon protein, itself is used to manufacture medicaments
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The
 CC treatment is contemplated for both human and animals, such as those
 CC important to the livestock industry. The antibody and polynucleotides are
 CC useful in diagnosis of conditions as above

SQ Sequence 33 AA;

Query Match 99.4%; Score 163; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33

Db 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33

RESULT 2

ADR43346

ID ADR43346 standard; peptide; 33 AA.

AC ADR43346;

DT 04-NOV-2004 (first entry)

DE Human Beacon protein.

XX Beacon; Anorectic; Anabolic; Antidiabetic; Cytostatic; Cardiant;
 KW Antinflammatory; Immunosuppressive; Antinfertility; Neuroprotective;
 KW Nootropic; CLK; myopathy; obesity; anorexia; diabetes; cancer;
 KW heart disease; inflammation; Alzheimer's; Parkinson's; Pearson Syndrome;
 KW Pyruvate Carboxylase Deficiency; Pyruvate Dehydrogenase Deficiency;
 KW Cancer; Acoustic Neuroma; Acute Lymphocytic Leukemia; Carcinoma;
 KW Leukemia.

XX Homo sapiens.

XX WO2004069866-A1.

XX 19-AUG-2004.

XX 10-FEB-2004; 2004WO-AU000147.

XX 10-FEB-2003; 2003US-0446191P.

XX (AUTO-) AUTOGEN RES PTY LTD.

PA (UYDE-) UNIV DEAKIN.

XX Collier G, Walder K, Kerr-Bayles L;

XX WPI; 2004-604412/58.

XX New isolated ligands of mammalian or avian Beacon, useful for e.g.

PT preventing or treating disorders associated with myopathy, obesity,

PT diabetes, cancer, heart disease, inflammation, or disorders associated

PT with the immune system.

XX Claim 3; SEQ ID NO 4; 194pp; English.

XX The present invention relates to an isolated ligand of mammalian or avian
 CC Beacon or a homolog or derivative of the Beacon. The composition
 CC (including the agent capable of modulating the interaction between a
 CC Beacon and a CLK) or methods are useful for manufacturing a medicament
 CC for the treatment of a condition characterized by a healthy or unhealthy
 CC state, including the presence or absence of a disorder associated with
 CC myopathy, obesity, anorexia, weight maintenance, diabetes, disorders
 CC associated with mitochondrial dysfunction, genetic disorders, cancer,
 CC heart disease, inflammation, disorders associated with the immune system,
 CC infertility, disease associated with the brain and/or metabolic energy
 CC levels. The disease is selected from Alzheimer's, Parkinson's, diabetes,
 CC autism, and the aging process, LIC (Lethal Infantile Cardiomyopathy),

CC abgr;-oxidation Defects, COX Deficiency, Mitochondrial Cytopathy, Alper's
 CC Disease, Barth Syndrome, Carnitine-Acyl-Carnitine Deficiency, Carnitine
 CC Deficiency, Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II
 CC Deficiency, Complex III Deficiency, Complex IV Deficiency, Complex V
 CC Deficiency, chronic progressive external ophthalmoplegia syndrome (CPEO),
 CC CPT I Deficiency, Glutaric Aciduria Type II, Kearns-Sayre syndrome (KSS),
 CC lactic acidosis, long-chain acyl-CoA dehydrogenase deficiency (LCAD),
 CC LCHAD, Leigh Disease, Leber Hereditary Optic Neuropathy (LHON), Luft
 CC Disease, mitochondrial DNA depletion, Mitochondrial Encephalopathy,
 CC Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase
 CC Deficiency, and the other diseases mentioned in the specification. The
 CC cancer is selected from ABL1 protooncogene, AIDS Related Cancers,
 CC Acoustic Neuroma, Acute Lymphocytic Leukemia, Acute Myeloid Leukemia,
 CC Adenocystic carcinoma, Adrenocortical Cancer, Agnogenic myeloid
 CC metaplasia, Alopecia, Alveolar soft-part sarcoma, Anal cancer,
 CC Angiosarcoma, Aplastic Anemia, Astrocytoma, Ataxia-telangiectasia, Basal
 CC Cell Carcinoma (Skin), Bladder Cancer, Bone Cancer, Bowel cancer, Brain
 CC Stem Glioma, Brain and CNS Tumours, Breast Cancer, CNS tumours, Carcinoid
 CC Tumours, Cervical Cancer, Childhood Brain Tumour, Childhood Cancer,
 CC Childhood Leukemia, and other cancers mentioned in the specification. The
 CC 11 sequences mentioned in the body of the specification do not correspond
 CC to the sequences represented in the SEQ ID listing.

XX SQ Sequence 33 AA;

Query Match 99.4%; Score 163; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33

Db 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33

RESULT 3

AA08413

ID AA08413 standard; protein; 73 AA.

XX AC AA08413;

XX 24-JUL-1999 (first entry)

XX P. obeus beacon protein.

XX Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;
 KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;
 KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;
 KW medicament; livestock; diagnosis.

XX Psammomys obesus.

XX WO9923217-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-AU000902.

XX 31-OCT-1997; 97AU-00000117.

XX 11-NOV-1997; 97AU-00000323.

XX (ITDI-) INT DIABETES INST.

XX (UYDE-) UNIV DEAKIN.

XX Zimmet PZ, Collier G;

XX WPI; 1999-337484/28.

XX N-PSDB; AAX57359.

XX New gene encoding a beacon protein associated with modulation of obesity,
 PT diabetes and metabolic energy levels.

XX Claim 2; Page 50; 85pp; English.

CC This invention describes a novel beacon protein and its encoding nucleic acid which is expressed in larger amounts in hypothalamus tissue of obese animals compared to lean animals. Agonists and antagonists of beacon can be used to treat obesity, anorexia, weight maintenance, energy imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin resistance. The beacon protein, itself is used to manufacture medicaments for treatment of obesity, anorexia, energy imbalance or diabetes. The treatment is contemplated for both human and animals, such as those important to the livestock industry. The antibody and polynucleotides are useful in diagnosis of conditions as above

XX Sequence 73 AA;

Query Match 99.4%; Score 163; DB 2; Length 73;

Best Local Similarity 97.0%; Pred. No. 2.2e-14;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

DB 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

RESULT 4

AAB36290

ID AAB36290 standard; protein; 73 AA.

XX AC

XX AAB36290;

XX 23-FEB-2001 (first entry)

XX DE Israeli sand rat beacon ligand.

XX Israel sand rat; beacon; obesity; NIDDM; energy balance; diabetes;

KW ligand.

XX Psammomys obesus.

XX WO20064931-A1.

XX 02-NOV-2000.

XX 19-APR-2000; 2000WO-AU000342.

XX 23-APR-1999; 99AU-00009919.

XX 24-MAR-2000; 2000AU-00006454.

XX (AUTO-) AUTOGEN PTY LTD.

XX Collier G, Walder K, Zimmet P;

XX WPI; 2000-687311/67.

XX N-PSDB; AAC81767.

XX Ligand of beacon protein useful for treating obesity, anorexia, energy

XX imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and

XX insulin resistance.

XX Claim 3; Fig 1; 67pp; English.

XX The present invention is related to the isolation of a ligand known as

XX beacon from the Israeli sand rat. Beacon is associated with the

XX regulation of energy balance, and the protein, its coding sequence and

XX analogues can be used in the treatment of diabetes, obesity, anorexia,

XX energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and

XX insulin resistance. In addition, they can be used in agriculture to

XX produce leaner animals

XX Sequence 73 AA;

Query Match 99.4%; Score 163; DB 3; Length 73;

Best Local Similarity 97.0%; Pred. No. 2.2e-14;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

DB 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

RESULT 4

AAB36290

ID AAB36290 standard; protein; 73 AA.

XX AC

XX AAB36290;

XX 23-FEB-2001 (first entry)

XX DE Israeli sand rat beacon ligand.

XX Israel sand rat; beacon; obesity; NIDDM; energy balance; diabetes;

KW ligand.

XX Psammomys obesus.

XX WO20064931-A1.

XX 02-NOV-2000.

XX 19-APR-2000; 2000WO-AU000342.

XX 23-APR-1999; 99AU-00009919.

XX 24-MAR-2000; 2000AU-00006454.

XX (AUTO-) AUTOGEN PTY LTD.

XX Collier G, Walder K, Zimmet P;

XX WPI; 2000-687311/67.

XX N-PSDB; AAC81767.

XX Ligand of beacon protein useful for treating obesity, anorexia, energy

XX imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and

XX insulin resistance.

XX Claim 3; Fig 1; 67pp; English.

XX The present invention is related to the isolation of a ligand known as

XX beacon from the Israeli sand rat. Beacon is associated with the

XX regulation of energy balance, and the protein, its coding sequence and

XX analogues can be used in the treatment of diabetes, obesity, anorexia,

XX energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and

XX insulin resistance. In addition, they can be used in agriculture to

XX produce leaner animals

XX Sequence 73 AA;

Query Match 99.4%; Score 163; DB 3; Length 73;

Best Local Similarity 97.0%; Pred. No. 2.2e-14;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

DB 1 MIEVVCNDRLGKKVVKCNTDDTIGDLKLLIAA 33

RESULT 5

AAM39680

ID AAM39680 standard; protein; 73 AA.

XX AC

XX AAM39680;

XX 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 2825.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX OS

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

XX Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI58836.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

XX as central nervous system injuries.

XX Example 4; SEQ ID NO 2825; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the

XX encoded polypeptides (AAM38642-AA42213) with nootropic,

XX immunosuppressant and cytostatic activity. The polynucleotides are useful

XX in gene therapy. A composition containing a polypeptide or polynucleotide

XX of the invention may be used to treat diseases of the peripheral nervous

XX system, such as peripheral nervous injuries, peripheral neuropathy and

XX localised neuropathies and central nervous system diseases, such as

XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

XX utilisation of the activities such as: immune system suppression,

XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,

XX assays for receptor activity, arthritis and inflammation, leukaemia and

XX C.N.S disorders. Note: The sequence data for this patent did not form

XX part of the printed specification

XX Sequence 73 AA;

Query Match 99.4%; Score 163; DB 4; Length 73;

CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 115 AA;

Query Match 99.4%; Score 163; DB 5; Length 115;
 Best Local Similarity 97.0%; Pred. No. 3.4e-14;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNCTDDTIGDLKKLIAA 33
 |||||
 DB 43 MIEVVCNDRLGKKVVKCNCTDDTIGDLKKLIAA 75

RESULT 8

ABB59910
 ID ABB59910 standard; protein; 73 AA.

XX AC ABB59910;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 6522.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL04013.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX PS Disclosure; SEQ ID NO 6522; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 73 AA;

Query Match 92.7%; Score 152; DB 4; Length 73;
 Best Local Similarity 87.9%; Pred. No. 6.7e-13;
 Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNCTDDTIGDLKKLIAA 33
 |||||
 DB 1 MIEITCNDRLGKKVVKCNPDPTIGDLKKLIAA 33

RESULT 9
 AAB36291
 ID AAB36291 standard; protein; 32 AA.
 XX AC AAB36291;

XX DT 23-FEB-2001 (first entry)

XX DE Human beacon (short form) protein sequence.

XX KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes;
 XX ligand; human.

XX OS Homo sapiens.

XX PN WO200064931-A1.

XX PD 02-NOV-2000.

XX PF 19-APR-2000; 2000WO-AU000342.

XX PR 23-APR-1999; 99AU-00009919.

XX PR 24-MAR-2000; 2000AU-00006454.

XX PA (AUTO-) AUTOGEN PTY LTD.

XX PI Collier G, Walder K, Zimmet P;

XX DR WPI; 2000-687311/67.

XX DR N-PSDB; AAC81770.

XX PT Ligand of beacon protein useful for treating obesity, anorexia, energy
 PT imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and
 PT insulin resistance.

XX PS Disclosure; Fig 1B; 67pp; English.

XX CC The present invention is related to the isolation of a ligand known as
 CC beacon from the Israeli sand rat. Beacon is associated with the
 CC regulation of energy balance, and the protein, its coding sequence and
 CC analogues can be used in the treatment of diabetes, obesity, anorexia,
 CC energy imbalance, metabolic syndrome, dyslipidemia, hypertension and
 CC insulin resistance. In addition, they can be used in agriculture to
 CC produce leaner animals

XX SQ Sequence 32 AA;

Query Match 89.9%; Score 147.5; DB 3; Length 32;
 Best Local Similarity 97.0%; Pred. No. 1.2e-12;
 Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MIEVVCNDRLGKKVVKCNCTDDTIGDLKKLIAA 33
 |||||
 DB 1 MIEVVCNDRLGKKVVKCNCTDDTIGDL-KLIAA 32

RESULT 10
 AAG40885
 ID AAG40885 standard; protein; 73 AA.
 XX AC AAG40885;

XX DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 50790.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
XX Zea mays subsp. mays.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 21-JUN-1999; 99US-0139817P.
DE 22-JUN-1999; 99US-0139899P.
XX 23-JUN-1999; 99US-0140353P.
XX 23-JUN-1999; 99US-0140354P.
KW 24-JUN-1999; 99US-0140695P.
KW 28-JUN-1999; 99US-0140823P.
XX 29-JUN-1999; 99US-0140991P.
XX 30-JUN-1999; 99US-0141287P.
XX 01-JUL-1999; 99US-0141842P.
XX 01-JUL-1999; 99US-0142154P.
PN 02-JUL-1999; 99US-0142055P.
XX 06-JUL-1999; 99US-0142390P.
XX 08-JUL-1999; 99US-0142803P.
XX 09-JUL-1999; 99US-0142920P.
XX 12-JUL-1999; 99US-0142977P.
XX 13-JUL-1999; 99US-0143542P.
XX 14-JUL-1999; 99US-0143624P.
XX 15-JUL-1999; 99US-0144005P.
XX 16-JUL-1999; 99US-0144085P.
XX 16-JUL-1999; 99US-0144086P.
XX 19-JUL-1999; 99US-0144325P.
XX 19-JUL-1999; 99US-0144331P.
XX 19-JUL-1999; 99US-0144332P.
XX 19-JUL-1999; 99US-0144333P.
XX 19-JUL-1999; 99US-0144334P.
XX 19-JUL-1999; 99US-0144335P.
XX 20-JUL-1999; 99US-0144352P.
XX 20-JUL-1999; 99US-0144632P.
XX 20-JUL-1999; 99US-0144884P.
XX 21-JUL-1999; 99US-0144814P.
XX 21-JUL-1999; 99US-0145086P.
XX 21-JUL-1999; 99US-0145088P.
XX 22-JUL-1999; 99US-0145085P.
XX 22-JUL-1999; 99US-0145087P.
XX 22-JUL-1999; 99US-0145089P.
XX 22-JUL-1999; 99US-0145192P.
XX 23-JUL-1999; 99US-0145145P.
XX 23-JUL-1999; 99US-0145218P.
XX 23-JUL-1999; 99US-0145224P.
XX 26-JUL-1999; 99US-0145276P.
XX 27-JUL-1999; 99US-0145913P.
XX 27-JUL-1999; 99US-0145918P.
XX 27-JUL-1999; 99US-0145919P.
XX 28-JUL-1999; 99US-0145951P.
XX 02-AUG-1999; 99US-0146386P.
XX 02-AUG-1999; 99US-0146388P.
XX 02-AUG-1999; 99US-0146389P.
XX 03-AUG-1999; 99US-0147038P.
XX 04-AUG-1999; 99US-0147204P.
XX 04-AUG-1999; 99US-0147302P.
XX 05-AUG-1999; 99US-0147192P.
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XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52222.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Best Local Similarity 84.8%; Pred. No. 2.1e-11; Mismatches 4; Indels 0; Gaps 0;
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Db 1 MIEVLCNDRLGKGVXVKNCDDTIGDLNKLVA 33

RESULT 14

ADT58384

ID ADT58384 standard; protein; 73 AA.

XX AC ADT58384;

XX DT 13-JAN-2005 (first entry)

XX DE Plant polypeptide, SEQ ID 8461.

XX KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX XX 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PR 28-APR-2003; 2003US-00425115.

XX PA (KOVA/) KOVALIC D K.

XX PI Kovalic DK;

XX DR WPI; 2004-757369/74.

XX PT New recombinant DNA constructs useful in the field of biochemistry and
PT Genetics, and in particular for producing transgenic plants with improved

PT biological characteristics.

PS Claim 2; SEQ ID NO 8461; 14pp; English.

XX

CC The invention relates a recombinant DNA construct comprising a

CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:

CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences

CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,

CC Arabidopsis, wheat and rape but the specification does not indicate which

CC sequences is derived from which organism. Also included is a method of

CC producing a plant having an improved property, comprising transforming a

CC plant with a recombinant DNA construct comprising a promoter region

CC functional in a plant cell operably joined to a polynucleotide encoding a

CC polypeptide associated with the property, and growing the transformed

CC plant. The property is selected from improving plant cold tolerance, for

CC manipulating growth rate in plant cells by modification of the cell cycle

CC pathway, for improving plant drought tolerance, for providing increased

CC resistance to plant disease, for galactomannan production, for production

CC of plant growth regulators, for improving plant heat tolerance, for

CC improving plant tolerance to herbicides, for increasing the rate of

CC homologous recombination in plants, for lignin production, for improving

CC plant tolerance to extreme osmotic conditions, for improving plant

CC tolerance to pathogens or pests, for yield improvement by modification of

CC photosynthesis, for modifying seed oil yield and/or content, for

CC modifying seed protein yield and/or content, for yield improvement by

CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake

CC and for yield improvement by providing improved plant growth and

CC development under at least one stress condition. The polynucleotide may

CC also encode a plant transcription factor. The methods and compositions of

CC the present invention are useful in the field of biochemistry and

CC genetics, in particular for producing transgenic plants with improved

CC biological characteristics such as increased yield, improved nitrogen

CC flow, increasing plant tolerance to cold or heat, improving plant

CC tolerance to extreme osmotic and drought conditions, and improving plant

CC tolerance to plant pests or pathogens. They can also be used in physical

CC arrays of molecules, plant breeding markers, computer-based storage and

CC analysis systems. The present sequence is one of the 5544 plant protein

CC sequences of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX

XX Sequence 73 AA;

QY Query Match 79.6%; Score 130.5; DB 8; Length 73;

Best Local Similarity 84.8%; Pred. No. 5.5e-10;

Matches 28; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MIEVVCNDRIGKVKVKNCTDDTIGDKKLIAA 33

DB 1 MIEVVLNDELGKVRVKC-XDTIGDKKLVA 32

RESULT 15

ADV95409

ID ADV95409 standard; peptide; 32 AA.

XX ADV95409;

AC ADV95409;

XX

XX 07-APR-2005 (first entry)

XX

XX Yeast ubiquitin like protein Hub1 amino terminal domain 1.

DE

XX Fusion protein; protein folding; protein structure;

KW ubiquitin like protein.

XX Saccharomyces cerevisiae.

OS

XX WO2005003313-A2.

PN

XX 13-JAN-2005.

XX

XX 28-JUN-2004; 2004WO-US020778.

PF

XX 26-JUN-2003; 2003US-0482817P.

XX (LIFE-) LIFESENSORS INC.

PA

XX Butt TR, Malakhov MP, Malakhova OA;

PI

XX WPI; 2005-091798/10.

DR

XX

XX Enhancing expression of target protein in host cell, by expressing

PT nucleic acid construct containing sequences encoding carboxy-terminal

PT domain of ubiquitin-like molecule and target protein and encoding fusion

PT protein in host cell.

XX

XX Example 7; SEQ ID NO 41; 107pp; English.

XX

CC The invention relates to enhancing (M1) the expression of a protein of

CC interest in a host cell, involving expressing a nucleic acid construct

CC comprising a nucleic acid sequence encoding a carboxy-terminal domain of

CC a ubiquitin-like (Ubl) molecule and a protein of interest, where the

CC presence of the carboxy-terminal domain of the Ubl molecule in the fusion

CC protein increases expression level of protein of interest in the host

CC cell. Also included are producing (M2) a protein of interest (involves

CC carrying out (M1), where the fusion protein, when expressed, comprises

CC the carboxy-terminal domain of Ubl molecule attached to the amino-

CC terminus of the protein of interest such that a cleavage site of the Ubl

CC molecule is immediately amino terminal to the protein of interest,

CC expressing the nucleic acid construct in the host cell, contacting the

CC expressed fusion protein with an amino-terminal domain of the same Ubl

CC molecule, thus generating a reconstituted Ubl, and contacting the

CC reconstituted Ubl with a protease specific to the Ubl molecule, thus

CC cleaving the fusion protein such that the protein of interest is now

CC produced), purifying (M3) the protein of interest (involving carrying out

CC (M2), purifying the reconstituted Ubl on a solid support capable of

CC specifically binding a purification tag (e.g. 6xHis tag or S-tag), and

CC contacting the purified reconstituted Ubl with a protease specific to the

CC Ubl molecule and cleaving the fusion protein such that the protein of

CC interest is now purified, or providing a nucleic acid construct which

CC encodes a fusion protein, containing a nucleic acid sequence encoding a

CC carboxy-terminal domain of Ubl molecule, the protein of interest, and a

CC first purification tag (attached to the amino-terminus of the carboxy-

CC terminal domain of a Ubl molecule) such that cleavage site of the Ubl

CC molecule is immediately amino terminal to the protein of interest,

CC expressing the nucleic acid construct encoding the fusion protein in the

CC host cell, purifying the fusion protein on a solid support capable of

CC specifically binding to the first purification tag, contacting the

CC purified fusion protein with an amino-terminal domain of the same Ubl

CC molecule comprising a second purification tag, thus generating a

CC reconstituted Ubl, purifying the reconstituted Ubl on a solid support

CC capable of specifically binding the second purification tag, and

CC contacting the purified reconstituted Ubl with a protease specific to the

CC Ubl molecule, thus cleaving the fusion protein such that the protein of

CC interest is now purified), increasing (M4) the affinity between a carboxy

CC -terminal domain of a Ubl molecule and an amino-terminal domain of a Ubl

CC molecule (involving operably linking a moiety to the carboxy-terminal and

CC to the amino-terminal domain, or inserting mutations into the carboxy-

CC terminal domain and the amino-terminal domain), a kit for purification of a

CC protein from a host cell, and generating an altered amino terminus in a

CC protein of interest in a host cell. The Ubl molecule is chosen from SUMO

CC (small ubiquitin related modifier), ubiquitin, RUB, HUB, APG8, APG12,

CC URM1, PART10, Ubi-L and ISG15, preferably SUMO. The purification tag is

CC chosen from polyhistidine tag (6x His), polyarginine tag, glutathione-S-

CC transferase (GST), maltose binding protein (MBP), S-tag, influenza virus

CC HA tag, thioredoxin, staphylococcal protein A tag, the FLAG epitope,

CC AviTag epitope, and the c-myc epitope. The methods are useful for

CC enhancing the expression of a protein of interest in a host cell chosen

CC from yeast cell, Escherichia coli, bacterial cell, mammalian cell and

CC insect cell. The yeast SUMO N terminus is designated NTHS (N-terminal

CC half of SUMO) and the C-terminus CTHS. The present sequence represents a

CC ubiquitin like protein (or its N- or C-terminus) suitable for use in a

CC fusion protein of the invention.

XX

XX Sequence 32 AA;

Query Match 69.5%; Score 114; DB 9; Length 32;
Best Local Similarity 65.6%; Pred. No. 4.1e-08;
Matches 21; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MIEVVNDRLGKKRVKCLAEBSVGDFFKKVLS 32

Search completed: March 29, 2006, 09:03:17
Job time : 82 secs

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Db 597 IKKNTDLDGDPFK 610

RESULT 8

AS3102

alpha-2-macroglobulin receptor precursor - chicken

NAlternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

CSpecies: Gallus gallus (chicken)

CDate: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

CAccession: AS3102

RNimf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A>Title: The somatic cell-specific low density lipoprotein receptor-related protein of b

AReference number: AS3102; MUID:94103212; PMID:7506255

AAccession: AS3102

AStatus: preliminary

A.Molecule type: mRNA

A.Residues: 1-4543 <NIM>

A.Cross-references: UNIPROT:P98157; UNIPARC:UPI000013C4B3; GB:X74904; NID:g438006; PIDN;

C.Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein.

C.Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C.Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro

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F.18-3942,3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <NAR>

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F.74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F.117-150/Domain: EGF homology <EG1>

F.156-190/Domain: EGF homology <EG2>

F.200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>

F.242-283/Domain: LDL receptor YWTD-containing repeat homology <YW02>

F.294-336/Domain: LDL receptor YWTD-containing repeat homology <YW03>

F.337-380/Domain: LDL receptor YWTD-containing repeat homology <YW04>

F.381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>

F.423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>

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F.1930-1972/Domain: LDL receptor YWTD-containing repeat homology <YW24>

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F.2016-2059/Domain: LDL receptor YWTD-containing repeat homology <YW26>

F.2060-2101/Domain: LDL receptor YWTD-containing repeat homology <YW27>

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F.2383-2423/Domain: LDL receptor YWTD-containing repeat homology <YW32>

F.2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>

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F.2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDL15>

F.2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDL16>

F.2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDL17>

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F.2983-3018/Domain: EGF homology <EG12>

F.3026-3065/Domain: LDL receptor YWTD-containing repeat homology <YW34>

F.3066-3110/Domain: LDL receptor YWTD-containing repeat homology <YW35>

F.3111-3153/Domain: LDL receptor YWTD-containing repeat homology <YW36>

F.3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW37>

F.3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW38>

F.3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>

F.3291-3327/Domain: EGF homology <EG13>

F.3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL18>

F.3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDL19>

F.3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDL20>

F.3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDL21>

F.3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDL22>

F.3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDL23>

F.3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDL24>

F.3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDL25>

F.3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDL26>

F.3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDL27>

F.3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDL28>

F.3783-3820/Domain: EGF homology <EG14>

F.3826-3858/Domain: EGF homology <EG15>

F.3866-3909/Domain: LDL receptor YWTD-containing repeat homology <YW40>

F.3910-3968/Domain: LDL receptor YWTD-containing repeat homology <YW41>

F.3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>

F.3943-4420/Domain: 85K chain extracellular #status predicted <EXT>

F.3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>

F.4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>

F.4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>

F.4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>

F.4150-4181/Domain: EGF homology <EG16>

F.4195-4230/Domain: EGF homology <EG17>

F.4235-4266/Domain: EGF homology <EG18>

F.4271-4302/Domain: EGF homology <EG19>

F.4307-4338/Domain: EGF homology <EG20>

F.4343-4373/Domain: EGF homology <EG21>

F.4376-4408/Domain: EGF homology <EG22>

F.4421-4443/Domain: transmembrane #status predicted <TM>

F.4444-4543/Domain: intracellular #status predicted <INT>

F.116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643

3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carboxydrate (Asn) (covalent)

F.168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F.2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 31.7%; Score 52; DB 1; Length 4543;

Best Local Similarity 41.7%; Pred. No. 2.1e+02;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVKCNDRLGKVKVKNCTDDTGD 26

DB 3655 EFQCNTLRKPLAWKCDGDDCGD 3678

RESULT 9

T31652

hypothetical protein Y57A10A.aa - Caenorhabditis elegans

CSpecies: Caenorhabditis elegans

CjDate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

CjAccession: T31652
RjSmyle, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z31048
A;Accession: T31652
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-201 <WIL>
A;Cross-references: UNIPARC:UPI000007BA8B, EMBL:AL117195; PIDN:CAB55035.1; CESP:Y57A10A.
A;Experimental source: clone Y57A10A
CjGenetics:
A;Gene: CESP:Y57A10A.see
A;Introns: 152/2
CjSuperfamily: translation initiation factor eIF-4E

Query Match 31.4%; Score 51.5; DB 2; Length 201;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 18; Conservative 5; Mismatches 7; Indels 9; Gaps 4;

QY 4 VVCNDR-LGKKVXV---KNTDPT---IGDL--KKLIAA 33
DB 124 LVCNVRGGGSKSVWTKNCNDDDTNMRIGVVLKSLMAA 162

RESULT 10

S42512
recombination-activating protein RAG-2 - rabbit
CjSpecies: Oryctolagus cuniculus (domestic rabbit)
CjDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
CjAccession: S42512; S42513; S42515; S42514
RjFuschiotti, P.; Harindranath, N.; Mage, R.G.; McCormack, W.T.; Dhanarajan, P.; Roux, K.
Mol. Immunol. 30, 1021-1032, 1993
A;Title: Recombination activating genes-1 and -2 of the rabbit: cloning and characterization
A;Reference number: S42511; MUID:93354283; PMID:8350872

A;Accession: S42512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-527 <FUS>
A;Cross-references: UNIPROT:P34089; UNIPARC:UPI000013308B, EMBL:W77667; NID:g165685; PIDN:AAA03028.1; PI
A;Accession: S42513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11,'1',13-15 <FU2>
A;Cross-references: UNIPARC:UPI000016CSB2; EMBL:M99310; NID:g165683; PIDN:AAA03028.1; PI
A;Accession: S42515
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 5-11,'1',13-113,'R',115-169,'K',171-350,'S',352-439,'R',441-527 <FU3>
A;Cross-references: UNIPARC:UPI000016CSB1; EMBL:M99312; NID:g165681; PIDN:AAA03027.1; PI
A;Accession: S42514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 5-11,'1',13-164,'S',166-324,'R',326-350,'S',352-527 <FU4>
A;Cross-references: UNIPARC:UPI000016CSB3; EMBL:M99311; NID:g165679; PIDN:AAA03026.1; PI
CjComment: This protein is required for immunoglobulin or T-cell receptor gene rearrange
CjSuperfamily: recombination-activating protein RAG-2

Query Match 31.1%; Score 51; DB 2; Length 527;
Best Local Similarity 37.0%; Pred. No. 44;
Matches 10; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 MIEVVCNDRLGKKVXVKCNTDPTIGDL 27
DB 109 VMSVVCKN--NKKVTFRCRDLVGDV 133

RESULT 11

T01857
hypothetical protein F9D12.1 - Arabidopsis thaliana
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjDate: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
CjAccession: T01857

RjMurray, J.; Langston, Y.; Ahrens, C.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of Arabidopsis thaliana F9D12.
A;Reference number: Z14444

A;Accession: T01857
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-662 <MUR>
A;Cross-references: UNIPROT:O81505; UNIPARC:UPI00000A7B91; EMBL:AF077407; NID:g3319339;
A;Experimental source: cultivar Columbia
CjGenetics:
A;Map position: 4
A;Introns: 63/1, 102/3, 126/2, 165/3, 194/3, 223/3, 249/2, 315/3, 362/1
A;Note: F9D12.1

Query Match 31.1%; Score 51; DB 2; Length 662;
Best Local Similarity 39.1%; Pred. No. 53;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 9 RLGGKKVXVKCNTDPTIGDLKKLI 31
DB 222 RQEKIVFTCCDDKVDIRLV 244

RESULT 12

T39553
vacuolar protein sorting-associated protein - fission yeast (Schizosaccharomyces pombe)
CjSpecies: Schizosaccharomyces pombe
CjDate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
CjAccession: T39553
RjPurnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21863
A;Accession: T39553
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3131 <PUR>
A;Cross-references: UNIPROT:O42926; UNIPARC:UPI000006AD1B; EMBL:AL021767; PIDN:CAA16910.
A;Experimental source: strain 972h-; cosmid c16C6
CjGenetics:
A;Gene: SPDB:SPBC16C6.02c
A;Map position: 2
A;Introns: 8/1, 45/3, 96/3; 2958/3

Query Match 31.1%; Score 51; DB 2; Length 3131;
Best Local Similarity 44.0%; Pred. No. 2e+02;
Matches 11; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 1 MIEVVCNDRLGKKVX--VKCNTDPT 23
DB 1873 VIEVVCNDRSGHRSQSSVIKIDPNET 1897

RESULT 13

S02392
alpha-2-macroglobulin receptor precursor - human
NjAlternate names: C991; LDL receptor-related protein 1; low density lipoprotein receptor
CjSpecies: Homo sapiens (man)
CjDate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
CjAccession: S02392; S30027; I37998; A39210; S12538
RjHeiz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.
EMBO J. 7, 4119-4127, 1988
A;Title: Surface location and high affinity for calcium of a 500-kd liver membrane prote
A;Reference number: S02392; MUID:89210795; PMID:3266596
A;Accession: S02392
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-4544 <HER>
A;Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:g34338; PIDN
RjKristensen, T.
submitted to the EMBL Data Library, October 1990
A;Reference number: S30027
A;Accession: S30027

A:Molecule type: mRNA
A:Residues: 3275-3864 <XRI>
A:Cross-references: UNIPARC:UPI00001736CD; EMBL:X55077
R:Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
EMBO J. 9, 1769-1776, 1990
A:Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein
A:Contents: annotation; site of proteolytic cleavage
A:Reference number: S12538; MUID:90269210; PMID:2112085
R:Kutt, H.; Herz, J.; Stanley, K.K.
Biochim. Biophys. Acta 1009, 229-236, 1989
A:Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promote
A:Reference number: I37998; MUID:90089395; PMID:2597675
A:Accession: I37998
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: UNIPARC:UPI0000000A1E; EMBL:X15424; NID:g34408; PIDN:CAA33464.1; PID
R:Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves, J.
J. Biol. Chem. 265, 17401-17404, 1990
A:Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip
A:Reference number: A39210; MUID:91009181; PMID:1698775
A:Accession: A39210
A>Status: preliminary
A:Molecule type: protein
A:Residues: 150-166/234-238, 'X', 240-245, 'X', 247-252, 'G', 686-695; 902-916; 1096-1109; 'S', 17
A:Cross-references: UNIPARC:UPI00001736CE; UNIPARC:UPI00001736CF; UNIPARC:UPI00001736D0;
GDS; UNIPARC:UPI00001736D6; UNIPARC:UPI00001736D7
C:Genetic:
A:Gene: GDB:LRPI; APR; LRP; A2MR
A:Cross-references: GDB:119694; OMIM:107770
A:Map position: 12q13.1-12q13.3
C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
clated protein (see PIR:A39875).
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C:Keywords: beta-hydroxyaspartic acid; calcium binding; glycopro
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-3943/Product: alpha-2-macroglobulin receptor 51K chain #status predicted <51K>
F:27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:115-148/Domain: EGF homology <EG1>
F:154-188/Domain: EGF homology <EG2>
F:198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F:240-281/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F:292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F:335-378/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F:379-420/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F:421-468/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F:478-519/Domain: EGF homology <EG3>
F:571-613/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F:614-659/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F:660-710/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F:711-752/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F:753-799/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F:807-842/Domain: EGF homology <EG4>
F:854-890/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:895-931/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:936-971/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:976-1011/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:1015-1051/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:1062-1097/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:1104-1140/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:1145-1182/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:1185-1221/Domain: EGF homology <EG5>
F:1227-1261/Domain: EGF homology <EG6>
F:1269-1308/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F:1309-1355/Domain: LDL receptor YWTD-containing repeat homology <YW13>
F:1356-1398/Domain: LDL receptor YWTD-containing repeat homology <YW14>
F:1399-1445/Domain: LDL receptor YWTD-containing repeat homology <YW15>
F:1446-1488/Domain: LDL receptor YWTD-containing repeat homology <YW16>
F:1489-1531/Domain: LDL receptor YWTD-containing repeat homology <YW17>
F:1540-1578/Domain: EGF homology <EG7>
F:1583-1626/Domain: LDL receptor YWTD-containing repeat homology <YW18>
F:1627-1669/Domain: LDL receptor YWTD-containing repeat homology <YW19>

F:1670-1713/Domain: LDL receptor YWTD-containing repeat homology <YW20>
F:1714-1753/Domain: LDL receptor YWTD-containing repeat homology <YW21>
F:1754-1796/Domain: LDL receptor YWTD-containing repeat homology <YW22>
F:1797-1846/Domain: LDL receptor YWTD-containing repeat homology <YW23>
F:1850-1886/Domain: EGF homology <EG8>
F:1934-1976/Domain: LDL receptor YWTD-containing repeat homology <YW24>
F:1977-2019/Domain: LDL receptor YWTD-containing repeat homology <YW25>
F:2020-2063/Domain: LDL receptor YWTD-containing repeat homology <YW26>
F:2064-2105/Domain: LDL receptor YWTD-containing repeat homology <YW27>
F:2106-2151/Domain: LDL receptor YWTD-containing repeat homology <YW28>
F:2152-2194/Domain: EGF homology <EG9>
F:2195-2241/Domain: LDL receptor YWTD-containing repeat homology <YW29>
F:2242-2284/Domain: LDL receptor YWTD-containing repeat homology <YW30>
F:2285-2328/Domain: LDL receptor YWTD-containing repeat homology <YW31>
F:2329-2372/Domain: LDL receptor YWTD-containing repeat homology <YW32>
F:2373-2416/Domain: EGF homology <EG10>
F:2417-2460/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F:2461-2504/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F:2505-2548/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F:2549-2592/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F:2593-2636/Domain: LDL receptor ligand-binding repeat homology <LDLF>
F:2637-2680/Domain: LDL receptor ligand-binding repeat homology <LDLG>
F:2681-2724/Domain: LDL receptor ligand-binding repeat homology <LDLH>
F:2725-2768/Domain: LDL receptor ligand-binding repeat homology <LDLI>
F:2769-2812/Domain: LDL receptor ligand-binding repeat homology <LDLJ>
F:2813-2856/Domain: LDL receptor ligand-binding repeat homology <LDLK>
F:2857-2899/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:2900-2943/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:2944-2987/Domain: EGF homology <EG11>
F:2988-3031/Domain: EGF homology <EG12>
F:3032-3075/Domain: LDL receptor YWTD-containing repeat homology <YW34>
F:3076-3119/Domain: LDL receptor YWTD-containing repeat homology <YW35>
F:3120-3163/Domain: LDL receptor YWTD-containing repeat homology <YW36>
F:3164-3207/Domain: LDL receptor YWTD-containing repeat homology <YW37>
F:3208-3251/Domain: LDL receptor YWTD-containing repeat homology <YW38>
F:3252-3295/Domain: EGF homology <EG13>
F:3296-3339/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:3340-3383/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:3384-3427/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:3428-3471/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:3472-3515/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:3516-3559/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:3560-3603/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:3604-3647/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:3648-3691/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:3692-3735/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:3736-3779/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:3780-3823/Domain: EGF homology <EG14>
F:3824-3867/Domain: EGF homology <EG15>
F:3868-3911/Domain: LDL receptor YWTD-containing repeat homology <YW40>
F:3912-3955/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F:3956-3999/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F:4000-4043/Domain: 85K chain extracellular #status predicted <EXT>
F:4044-4087/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F:4088-4131/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F:4132-4175/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F:4176-4219/Domain: EGF homology <EG16>
F:4220-4263/Domain: EGF homology <EG17>
F:4264-4307/Domain: EGF homology <EG18>
F:4308-4351/Domain: EGF homology <EG19>
F:4352-4395/Domain: EGF homology <EG20>
F:4396-4439/Domain: EGF homology <EG21>
F:4440-4483/Domain: EGF homology <EG22>
F:4484-4527/Domain: transmembrane #status predicted <TM>
F:4528-4571/Domain: intracellular #status predicted <INT>
F:4572-4615/Domain: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:4616-4659/Domain: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:4660-4703/Domain: carbohydrate (Asn) (covalent) #status predicted
F:4704-4747/Domain: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.1%; Score 51; DB 1; Length 4544;
Best Local Similarity 41.7%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 10;


```

QY      3 EVVCDRLGKKVXKCNFTDITGD 26
bb      3659 EFQCNNTLCKPLAWKCDGEDDCG 3682

RESULT 15
A25161
tray protein - Salmonella typhimurium plasmid pSD208
C;Species: Salmonella typhimurium
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Feb-1997
C;Accession: A25161
R;Finlay, B.B.; Frost, L.S.; Paranchych, W.
J;Bacteriol 168, 990-998, 1986
A;Title: Nucleotide sequence of the trvAUS region from IncFV plasmid pSD208.
A;Reference number: A91828; MUID:87056998; PMID:2877970
A;Molecule type: DNA
A;Residues: 1-69 <FIN>
A;Cross-references: UNIPARC:UPI00001376DF
C;Genetics:
A;Gene: tray
A;Genome: plasmid
C;Keywords: DNA binding

Query Match      30.5%; Score 50; DB 2; Length 69;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      10 LGKKVXKCNFTDITGD 27
Db      10 IGKKNISCSLDAIDEL 27

```

Search completed: March 29, 2006, 09:07:57
Job time : 41 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:07:30 ; Search time 46 Seconds
(without alignments)
59.311 Million cell updates/sec

Title: US-10-067-832D-14
Perfect score: 164
Sequence: 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/R8_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	99.4	33	2 US-09-331-930A-14	Sequence 14, Appl
2	163	99.4	73	2 US-09-331-930A-2	Sequence 2, Appl
3	163	99.4	73	2 US-09-331-930A-19	Sequence 19, Appl
4	163	99.4	73	2 US-09-331-930A-20	Sequence 20, Appl
5	163	99.4	73	2 US-09-331-930A-21	Sequence 21, Appl
6	163	99.4	73	2 US-09-331-930A-24	Sequence 24, Appl
7	163	99.4	73	2 US-09-331-930A-25	Sequence 25, Appl
8	135	82.3	73	2 US-09-331-930A-22	Sequence 22, Appl
9	106	64.6	66	2 US-09-331-930A-23	Sequence 23, Appl
10	106	64.6	75	2 US-09-348-796A-16302	Sequence 16302, A
11	52	31.7	231	2 US-09-107-532A-5301	Sequence 5301, Ap
12	52	31.7	1094	2 US-09-268-347-32	Sequence 32, Appl
13	51	31.1	4544	1 US-08-469-486-52	Sequence 52, Appl
14	51	31.1	4544	1 US-08-469-658-52	Sequence 52, Appl
15	50	30.5	482	2 US-09-270-767-43292	Sequence 43292, A
16	49	29.9	113	2 US-09-173-300-54	Sequence 54, Appl
17	49	29.9	113	2 US-10-027-450-54	Sequence 54, Appl
18	49	29.9	347	2 US-09-370-767-57323	Sequence 57323, A
19	49	29.9	348	2 US-09-248-796A-18141	Sequence 18141, A
20	49	29.9	349	2 US-09-270-767-42065	Sequence 42065, A
21	48	29.3	359	2 US-09-516-143A-4	Sequence 4, Appl
22	48	29.3	359	2 US-09-984-205-4	Sequence 4, Appl
23	48	29.3	359	2 US-10-759-277-4	Sequence 4, Appl
24	48	29.3	359	2 US-09-930-440C-6	Sequence 6, Appl
25	48	29.3	367	2 US-09-949-016-9749	Sequence 9749, Ap
26	48	29.3	1070	2 US-09-107-532A-6735	Sequence 6735, Ap
27	47.5	29.0	883	2 US-09-348-796A-20980	Sequence 20980, A

28	47	28.7	193	2	US-08-671-548C-16	Sequence 16, Appl
29	47	28.7	193	2	US-08-284-667A-16	Sequence 16, Appl
30	47	28.7	262	2	US-09-328-352-5050	Sequence 5050, Ap
31	46	28.0	455	2	US-09-221-235-5	Sequence 5, Appl
32	46	28.0	455	2	US-09-221-928-5	Sequence 5, Appl
33	46	28.0	455	2	US-09-221-527-5	Sequence 5, Appl
34	46	28.0	455	2	US-09-221-236-5	Sequence 5, Appl
35	46	28.0	455	2	US-09-221-416-5	Sequence 5, Appl
36	46	28.0	455	2	US-09-221-245-5	Sequence 5, Appl
37	46	28.0	455	2	US-09-163-115-5	Sequence 5, Appl
38	46	28.0	455	2	US-09-221-528-5	Sequence 5, Appl
39	46	28.0	455	2	US-09-593-553-5	Sequence 5, Appl
40	46	28.0	455	2	US-09-221-237-5	Sequence 5, Appl
41	46	28.0	455	2	US-09-399-588-2	Sequence 2, Appl
42	46	28.0	455	2	US-09-757-982-5	Sequence 5, Appl
43	46	28.0	532	1	US-08-481-337A-6	Sequence 6, Appl
44	46	28.0	532	2	US-09-382-256-6	Sequence 6, Appl
45	46	28.0	532	2	US-09-382-256-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-331-930A-14
; Sequence 14, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OP INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: variable amino acid
US-09-331-930A-14

Query Match 99.4%; Score 163; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.2e-16; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33
|||||
DB 1 MIEVVCNDRLGKKVXVKCNTDTIGDLKKLIAA 33

RESULT 2
US-09-331-930A-2
; Sequence 2, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902

```

: GENERAL INFORMATION:
:
: APPLICANT: ZIMMET, PAUL Z.
: APPLICANT: COLLIER, GREGORY
:
: TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
:
: FILE REFERENCE: 22975-20007.00
:
: CURRENT APPLICATION NUMBER: US/09/331,930A
: CURRENT FILING DATE: 1999-06-30
:
: PRIOR APPLICATION NUMBER: PCT/AU98/00902
:
: PRIOR FILING DATE: 1998-10-30
:
: PRIOR APPLICATION NUMBER: AU FP0117/97
:
: PRIOR FILING DATE: 1997-10-31
:
: PRIOR APPLICATION NUMBER: AU FP0323/97
:

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; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-331-930A-24

Query Match 99.4%; Score 163; DB 2; Length 73;
Best Local Similarity 97.0%; Pred. No. 1.2e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVVKCNTDDTIGDLKKLIAA 33
|||:|||||:|||||:|||||:|||||:|||||
DB 1 MIEVNCNDRLGKKVVKCNTDDTIGDLKKLIAA 33

RESULT 7
US-09-331-930A-25
; Sequence 25, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-331-930A-25

Query Match 99.4%; Score 163; DB 2; Length 73;
Best Local Similarity 97.0%; Pred. No. 1.2e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVVKCNTDDTIGDLKKLIAA 33
|||:|||||:|||||:|||||:|||||:|||||
DB 1 MIEVNCNDRLGKKVVKCNTDDTIGDLKKLIAA 33

RESULT 8
US-09-331-930A-22
; Sequence 22, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 73

; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-331-930A-22

Query Match 82.3%; Score 135; DB 2; Length 73;
Best Local Similarity 78.8%; Pred. No. 9.6e-12;
Matches 26; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVVKCNTDDTIGDLKKLIAA 33
|||:|||||:|||||:|||||:|||||:|||||
DB 1 MIEITVNDRLGKKVRIKCNPSDTIGDLKKLIAA 33

RESULT 9
US-09-331-930A-23
; Sequence 23, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Fasciola hepatica
US-09-331-930A-23

Query Match 64.6%; Score 106; DB 2; Length 66;
Best Local Similarity 80.8%; Pred. No. 9.8e-08;
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 DRLGKKVVKCNTDDTIGDLKKLIAA 33
|||:|||||:|||||:|||||:|||||:|||||
DB 1 DRLGKKVVKCNTDKVGLKKLIAA 26

RESULT 10
US-09-248-796A-16302
; Sequence 16302, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16302
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16302

Query Match 64.6%; Score 106; DB 2; Length 75;
Best Local Similarity 61.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MIEVVCNRLGKKVXVKCNTDDTIGDLKLI	31
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Db	3	MIEIQNRLGKKIKLKCLETDTIGDVKKIL	33

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RESULT 12

US-09-268-347-32

Sequence 32, Application US/09268347

Patent No. 6335182

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.

TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS

FILE REFERENCE: 1038-860

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; CURRENT APPLICATION NUMBER: US/09/268,347
;
; CURRENT FILING DATE: 1999-03-16
;
; NUMBER OF SEQ ID NOS: 54
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 32
;
; LENGTH: 1094
;
; TYPE: PRT
;
; ORGANISM: Haemophilus influenzae
US-09-268-347-32

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RESULT 13
US-08-469-486-52
; Sequence 52, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegersen, Hans Christian
; APPLICANT: Holtet, Thor Lae
; APPLICANT: Esterodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-486-52

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Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 14

US-08-469-658-52
; Sequence 52, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Eterodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-658-52

Query Match 31.1%; Score 51; DB 1; Length 4544;
Best Local Similarity 41.7%; Pred. No. 3.7e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVCDRLGKGVKVCNTDDTIGD 26

Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681

RESULT 15

US-09-270-767-43292
; Sequence 43292, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43292
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43292

Query Match 30.5%; Score 50; DB 2; Length 482;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 13 KVVVKCNTDDTIGDLKKLI 31
DB 406 KTFVKCNKKEQKDLKKLI 424

Search completed: March 29, 2006, 09:08:49
Job time : 47 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:08:10 ; Search time 165 Seconds
(without alignments)
83.566 Million cell updates/sec

Title: US-10-067-832D-14
Perfect score: 164
Sequence: 1 MIEVVCNDRLGKKVVKCNTDTIGDLKKLIAA 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:
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4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	99.4	33	US-10-067-832D-14	Sequence 14, Appl
2	163	99.4	68	US-10-424-599-250542	Sequence 250542,
3	163	99.4	73	US-10-067-832D-2	Sequence 2, Appl
4	163	99.4	73	US-10-067-832D-15	Sequence 15, Appl
5	163	99.4	73	US-10-067-832D-16	Sequence 16, Appl
6	163	99.4	73	US-10-067-832D-19	Sequence 19, Appl
7	163	99.4	73	US-10-067-832D-20	Sequence 20, Appl
8	163	99.4	73	US-10-067-832D-68	Sequence 68, Appl
9	163	99.4	115	US-10-264-049-2463	Sequence 2463, Ap
10	152	92.7	73	US-11-097-143-6522	Sequence 6522, Ap
11	146	89.0	73	US-10-424-599-212296	Sequence 212296,
12	146	89.0	73	US-10-437-963-147593	Sequence 147593,
13	146	89.0	73	US-10-767-701-46049	Sequence 46049, A
14	146	89.0	73	US-10-425-115-233843	Sequence 233843,
15	146	89.0	73	US-10-425-115-233846	Sequence 233846,
16	146	89.0	73	US-10-425-115-233848	Sequence 233848,
17	146	89.0	73	US-10-425-115-233849	Sequence 233849,
18	146	89.0	73	US-10-425-115-233851	Sequence 233851,
19	146	89.0	73	US-10-425-115-233853	Sequence 233853,
20	146	89.0	73	US-10-425-115-288480	Sequence 288480,
21	146	89.0	73	US-10-425-115-288482	Sequence 288482,
22	146	89.0	73	US-10-425-115-288483	Sequence 288483,
23	146	89.0	73	US-10-425-115-288486	Sequence 288486,
24	140	85.4	73	US-10-425-115-288481	Sequence 288481,
25	137	83.5	73	US-10-425-115-288479	Sequence 288479,
26	135	82.3	73	US-10-067-832D-17	Sequence 17, Appl
27	134	81.7	89	US-10-425-115-355452	Sequence 355452,

28	131.5	80.2	74	4	US-10-424-599-207467	Sequence 207467,
29	130.5	79.6	73	5	US-10-739-930-8461	Sequence 8461, Ap
30	120	73.2	45	4	US-10-425-115-282612	Sequence 282612,
31	118	72.0	71	4	US-10-424-599-147197	Sequence 147197,
32	114	69.5	89	4	US-10-083-357-770	Sequence 770, App
33	114	69.5	320	4	US-10-338-411-11	Sequence 11, Appl
34	114	69.5	320	4	US-10-389-640-11	Sequence 11, Appl
35	111	67.7	82	4	US-10-424-599-191611	Sequence 191611,
36	110	67.1	73	4	US-10-425-115-230033	Sequence 230033,
37	106	64.6	66	5	US-10-067-832D-18	Sequence 18, Appl
38	97	59.1	55	4	US-10-425-115-270723	Sequence 270723,
39	97	59.1	110	4	US-10-424-599-213543	Sequence 213543,
40	93	56.7	83	4	US-10-437-963-135926	Sequence 135926,
41	84	51.2	59	4	US-10-425-115-356308	Sequence 356308,
42	84	51.2	79	4	US-10-425-115-269824	Sequence 269824,
43	68	41.5	27	3	US-09-864-761-41766	Sequence 41766, A
44	63	38.4	63	4	US-10-425-115-201973	Sequence 201973,
45	60	36.6	64	4	US-10-424-599-271299	Sequence 271299,

ALIGNMENTS

RESULT 1
US-10-067-832D-14
; Sequence 14, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: Leu, Pro, His, or Arg
US-10-067-832D-14

Query Match 99.4%; Score 163; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVVKCNTDTIGDLKKLIAA 33
Db 1 MIEVVCNDRLGKKVVKCNTDTIGDLKKLIAA 33

RESULT 2
US-10-424-599-250542
; Sequence 250542, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250542
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6826C.1.pap
US-10-424-599-250542

Query Match 99.4%; Score 163; DB 4; Length 68;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33
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DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 3

US-10-067-832D-2
; Sequence 2, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Peammomy obesus
US-10-067-832D-2

Query Match 99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33
|||||
DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 4

US-10-067-832D-15
; Sequence 15, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-832D-15

Query Match 99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33
|||||
DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 5

US-10-067-832D-16
; Sequence 16, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-832D-16

Query Match 99.4%; Score 163; DB 5; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.9e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33
|||||
DB 1 MIEVVCNDRLGKVKVVKCNTDDTIGDLKGLIAA 33

RESULT 6

US-10-067-832D-19
; Sequence 19, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117

Db 43 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 75
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RESULT 10
US-11-097-143-6522
; Sequence 6522, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6522
; LENGTH: 73
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6522

Query Match 92.7%; Score 152; DB 6; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.7e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33
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Db 1 MIEITCNDRLGKVKVCKNPDGTGDLKGLIAA 33
|||||

RESULT 11
US-10-424-599-212296
; Sequence 212296, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212296
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33729C.1.pep
US-10-424-599-212296

Query Match 89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33
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Db 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLVAA 33
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RESULT 12
US-10-437-963-147593
; Sequence 147593, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147593
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48107C.1.pep
US-10-437-963-147593

Query Match 89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33
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Db 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLVAA 33
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RESULT 13
US-10-767-701-46049
; Sequence 46049, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46049
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C594_1.pep
US-10-767-701-46049

Query Match 89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDGTGDLKGLIAA 33
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Db      1 MIEVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33
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RESULT 14
US-10-425-115-233843
; Sequence 233843, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233843
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144858C.1.pap
US-10-425-115-233843

Query Match      89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 MIEVNCNDRLGKKVVKCNEDDTIGDLKKLVAA 33
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Db      1 MIEVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33

RESULT 15
US-10-425-115-233846
; Sequence 233846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233846
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144860C.1.pap
US-10-425-115-233846

Query Match      89.0%; Score 146; DB 4; Length 73;
Best Local Similarity 87.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 MIEVNCNDRLGKKVVKCNEDDTIGDLKKLVAA 33
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MIEVLNDRLGKKVVKCNEDDTIGDLKKLVAA 33

Search completed: March 29, 2006, 09:11:39
Job time : 165 secs
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSs have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rwp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17311
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc_feature
; LOCATION: (1)..(375)
; OTHER INFORMATION: Ceres Seq. ID no. 12357280
US-11-096-568A-17311

Query Match      30.5%; Score 50; DB 7; Length 375;
Best Local Similarity 40.0%; Pred. No. 6;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY      2 IEVVCNDRLGKKVXKVCNTDDTTGDLKKLI 31
Db      154 IDLYOHRIDKKVPPIEV---TIGELKKLV 179

RESULT 8
US-11-004-399-3161
; Sequence 3161, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiekumar
; APPLICANT: Foon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3161
; LENGTH: 47
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-3161

Query Match      29.3%; Score 48; DB 7; Length 47;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 4; Mismatches 3; Indels 3; Gaps 0;

QY      16 VKCNTDDTTGDLKK 29
Db      23 IDCNTDVTSSLQK 36

RESULT 9
US-11-123-013-6
; Sequence 6, Application US/11123013
; Publication No. US20050287637A1
; GENERAL INFORMATION:
; APPLICANT: Betenbaugh, Michael J.
; APPLICANT: Lawrence, Shawn J.
; APPLICANT: Lee, Yuan C.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: Engineering Intracellular Sialylation Pathways
; FILE REFERENCE: 03940077bp
; CURRENT APPLICATION NUMBER: US/11/123,013
; CURRENT FILING DATE: 2005-05-06
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; PRIOR APPLICATION NUMBER: US 60/122,582
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/169,624
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/227,579
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/516,793
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/930,440
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-123-013-6

Query Match      29.3%; Score 48; DB 7; Length 359;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 EVVCNDRLGKKVXVK 17
Db      284 EMACNEKLGKSVYAK 298

RESULT 10
US-11-096-568A-31955
; Sequence 31955, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31955
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION: (1)..(114)
; OTHER INFORMATION: Ceres Seq. ID no. 13591797
US-11-096-568A-31955

Query Match      28.7%; Score 47; DB 7; Length 114;
Best Local Similarity 36.8%; Pred. No. 4.4;
Matches 14; Conservative 4; Mismatches 6; Indels 14; Gaps 3;

QY      1 MIEVVCNDRLGKKVXV-----KC-----NTDDTIG 25
Db      78 MVQILCND-CGKAEVQVHVVAQKCPNCKSYNTRQTRG 114

RESULT 11
US-11-096-568A-31954
; Sequence 31954, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31954
; LENGTH: 175
; TYPE: PRT
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-107

Query Match      31.1%; Score 51; DB 6; Length 37;
Best Local Similarity 41.7%; Pred. No. 0.31;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKKVXVKCNTDDTTIGD 26
| | | | | | | | | | | | | | | | | | | | |
Db 5 EFQCNNTLCKPLAWKCDGEDDCGD 28
| | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-10-501-035-214
; Sequence 214, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-214

Query Match      31.1%; Score 51; DB 6; Length 4544;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKKVXVKCNTDDTTIGD 26
| | | | | | | | | | | | | | | | | | | | |
Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681
| | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-32

Query Match      31.1%; Score 51; DB 7; Length 4544;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 EVVQNDRLGKKVXVKCNTDDTTIGD 26
| | | | | | | | | | | | | | | | | | | | |
Db 3658 EFQCNNTLCKPLAWKCDGEDDCGD 3681
| | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-11-096-568A-17313
; Sequence 17313, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17313
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(319)
; OTHER INFORMATION: Ceres Seq. ID no. 12357282
US-11-096-568A-17313

Query Match      30.5%; Score 50; DB 7; Length 319;
Best Local Similarity 40.0%; Pred. No. 5;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 ISVQNDRLGKKVXVKCNTDDTTIGDLKKLI 31
| | | | | | | | | | | | | | | | | | | | |
Db 98 IDLYYQHRIDKKVPIEV---TIGELKKLV 123
| | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-11-096-568A-17312
; Sequence 17312, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17312
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(346)
; OTHER INFORMATION: Ceres Seq. ID no. 12357281
US-11-096-568A-17312

Query Match      30.5%; Score 50; DB 7; Length 346;
Best Local Similarity 40.0%; Pred. No. 5.4;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 ISVQNDRLGKKVXVKCNTDDTTIGDLKKLI 31
| | | | | | | | | | | | | | | | | | | | |
Db 125 IDLYYQHRIDKKVPIEV---TIGELKKLV 150
| | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-11-096-568A-17311
; Sequence 17311, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17311
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(346)
; OTHER INFORMATION: Ceres Seq. ID no. 12357281
US-11-096-568A-17311

Query Match      30.5%; Score 50; DB 7; Length 346;
Best Local Similarity 40.0%; Pred. No. 5.4;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 ISVQNDRLGKKVXVKCNTDDTTIGDLKKLI 31
| | | | | | | | | | | | | | | | | | | | |
Db 125 IDLYYQHRIDKKVPIEV---TIGELKKLV 150
| | | | | | | | | | | | | | | | | | | | |
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US-10-957-351-107

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:09:05 ; Search time 25 Seconds
(without alignments)
40.183 Million cell updates/sec

Title: US-10-067-832D-14

Perfect score: 164

Sequence: 1 MIEVNCNDRLGKVKVVCNTDITGDKLKLIAA 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.5	34.5	258	7	US-11-058-924-6
2	51	31.1	37	6	US-10-957-351-107
3	51	31.1	4544	6	US-10-501-035-214
4	51	31.1	4544	7	US-11-076-427A-32
5	50	30.5	319	7	US-11-096-568A-17313
6	50	30.5	346	7	US-11-096-568A-17312
7	50	30.5	375	7	US-11-096-568A-17311
8	48	29.3	47	7	US-11-004-399-3161
9	48	29.3	359	7	US-11-123-013-6
10	47	28.7	114	7	US-11-096-568A-31955
11	47	28.7	175	7	US-11-096-568A-31954
12	47	28.7	250	7	US-11-096-568A-30582
13	47	28.7	258	7	US-11-096-568A-30581
14	47	28.7	272	7	US-11-096-568A-30580
15	47	28.7	286	7	US-11-096-568A-31559
16	47	28.7	294	7	US-11-096-568A-31558
17	47	28.7	308	7	US-11-096-568A-31557
18	47	28.7	355	7	US-11-087-099-3295
19	47	28.7	594	7	US-11-096-568A-31265
20	47	28.7	610	7	US-11-096-568A-31264
21	47	28.7	640	7	US-11-096-568A-31263
22	46	28.0	247	7	US-11-096-568A-29306
23	46	28.0	256	7	US-11-096-568A-29305
24	46	28.0	311	7	US-11-096-568A-29304
25	46	28.0	314	7	US-11-096-568A-19764

Sequence 19763, A
Sequence 19762, A
Sequence 7, Appli
Sequence 2800, Ap
Sequence 15, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 143, App
Sequence 1800, Ap
Sequence 354, App
Sequence 186, App
Sequence 684, App
Sequence 114, App
Sequence 8262, Ap
Sequence 16796, A
Sequence 16795, A
Sequence 16794, A
Sequence 21, Appl
Sequence 5, Appl

337 7 US-11-096-568A-19763
342 7 US-11-096-568A-19762
532 6 US-10-860-501-7
181 7 US-11-072-512-2800
313 7 US-11-087-719-15
323 7 US-11-087-719-14
338 7 US-11-087-719-13
339 6 US-10-821-234-1507
339 7 US-11-072-175-143
343 7 US-11-096-568A-1800
403 7 US-11-074-176-354
408 7 US-11-074-176-186
573 6 US-10-467-657-684
107 7 US-11-217-919-114
207 6 US-10-467-657-8262
316 7 US-11-096-568A-16796
336 7 US-11-096-568A-16795
341 7 US-11-096-568A-16794
450 7 US-11-109-156-21
450 7 US-11-230-995-5

ALIGNMENTS

RESULT 1
US-11-058-924-6
; Sequence 6, Application US/11058924
; Publication No. US20060019308A1
; GENERAL INFORMATION:
; APPLICANT: Lund, Frances E.
; APPLICANT: Randall, Troy D.
; TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
; FILE REFERENCE: 13315/5
; CURRENT APPLICATION NUMBER: US/11/058,924
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 09/982,616
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/241,065
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 258
; TYPE: PRT
; ORGANISM: A. californica
US-11-058-924-6

Query Match 34.5%; Score 56.5; DB 7; Length 258;
Best Local Similarity 37.5%; Pred. No. 0.41;
Matches 12; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
QY 2 IFVNCNDRLGKVKVVCNTDITGDKLKLIAA 33
DB 190 VKVIVLHRLGKIIKCCGAGSLL-DLEKLIVA 220
::: |||::|: ||: |||::|:
RESULT 2
US-10-957-351-107
; Sequence 107, Application US/10957351
; Publication No. US20060000844A1
; GENERAL INFORMATION:
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 09:02:15 ; Search time 230 Seconds
(without alignments)
101.228 Million cell updates/sec

Title: US-10-067-832D-14

Perfect score: 164

Sequence: 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKKLIAA 33

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	163	99.4	47	2	Q5BJSI_RAT
2	163	99.4	73	1	UBJ5_HUMAN
3	163	99.4	73	1	UBJ5_MESAU
4	163	99.4	73	1	UBJ5_MOUSE
5	163	99.4	73	1	UBJ5_PSAOB
6	163	99.4	73	2	Q5RCIO_PONPY
7	163	99.4	73	2	Q4R5J3_MACFA
8	153	93.3	73	1	UBJ5_BRARE
9	152	92.7	73	1	UBJ5_DROME
10	151	92.1	73	2	Q5H2C1_XENLA
11	150	91.5	73	2	Q7QHM2_ANOGA
12	147	89.6	73	2	Q4SM16_TETNG
13	146	89.0	73	1	UBJ5_ARATH
14	146	89.0	73	2	Q6K220_ORYSA
15	146	89.0	73	2	Q57QV8_ARATH
16	143	87.2	73	2	Q81545_PLAP7
17	143	87.2	73	2	Q7RBM4_PLAYO
18	143	87.2	73	2	Q4YUJ7_PLABE
19	142	86.6	73	2	Q9MIU1_ARATH
20	140	85.4	73	1	HUB1_SCHPO
21	136	82.9	87	2	Q54Q03_DICD1
22	135	82.3	73	1	UBJ5_CAEEL
23	135	82.3	73	2	Q617M9_CAEER
24	133	81.1	73	2	Q4P9W2_USTWA
25	133	81.1	73	2	Q4MZ69_THERPA
26	133	81.1	76	2	Q4UBB9_THERAN
27	131	79.9	73	2	Q5BS57_SCHJA
28	130	79.3	70	2	Q6CI04_YARLI
29	128	78.0	73	2	Q4VAF8_MOUSE
30	121	73.8	276	2	Q5KM54_CRYNE
31	121	73.8	276	2	Q5K8L5_CRYNE

32	120	73.2	73	1	HUB1_DEBHA	Q6bup7 debaromyce
33	117	71.3	73	1	HUB1_CANGA	Q6fix7 candida gla
34	116	70.7	74	1	HUB1_KLULA	Q6cu12 kluyveromyc
35	116	70.7	79	2	Q6CUI1_KLULA	Q6cu11 kluyveromyc
36	115	70.1	73	1	HUB1_ASHGO	Q756x3 ashbya gos
37	110	67.1	73	1	HUB1_YEAST	Q6Q546 saccharomyc
38	96	58.5	79	2	Q5OP03_ENTHI	Q50p03 entamoeba h
39	86	52.4	616	2	Q5BCG2_EMENI	Q5bcg2 aspergillus
40	85	51.8	237	2	Q41016_GIBZE	Q41016 gibberella
41	69	42.1	239	2	Q52620_MAGGR	Q52620 magnaporthe
42	62	37.8	189	2	Q4WYK6_ASFFU	Q4wyk6 aspergillus
43	62	37.8	261	2	Q8X065_NEUCR	Q8x065 neurospora
44	57	34.8	166	2	Q4WMP3_ASFFU	Q4wmp9 aspergillus
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ALIGNMENTS

RESULT 1

Q5BJSI_RAT

ID Q5BJSI_RAT PRELIMINARY; PRT; 47 AA.

AC Q5BJSI_

DT 10-MAY-2005 (Tremblrel. 30, Created)

DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE LOC500954 protein.

GN Name=LOC500954;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC091358; AAH91358.1; -; mRNA.

DR SMR; Q5BJSI; 1-47.

SQ SEQUENCE 47 AA; 5400 MW; B8PE50E31B325338 CRC64;

Query Match 99.4%; Score 163; DB 2; Length 47;

Best Local Similarity 97.0%; Pred. No. 2.9e-15;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKKLIAA 33

DB 1 MIEVVCNDRLGKKVXKNCNTDDTIGDLKKLIAA 33

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CC removed.
CC -----
CC EMBL; AF3131915; AAK314178.1; -; mRNA.
CC EMBL; BT007355; AAP36019.1; -; mRNA.
CC EMBL; BC007053; AAH07053.1; -; mRNA.
CC PDB; 1FOR; NMR; AA=1-73.
CC DR Ensembl; ENSG00000198258; Homo sapiens.
CC DR HGNC; HGNC:13736; UBL5.
CC DR H-InvDB; HIX0014729; -.
CC DR MIM; 606849; -.
CC DR GO; GO:0005737; C:cytoplasm; IDA.
CC DR InterPro; IPR000626; Ubiquitin.
CC DR Pfam; PF00240; ubiquitin; 1.
CC DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
CC DR PROSITE; PS00053; UBIQUITIN_2; FALSE NEG.
CC DR 3D-structure; Ubl conjugation pathway.
CC KW DOMAIN 1 73 Ubiquitin-like.
CC SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKGVKVCNTDGTIGDLKLLIAA 33
Db 1 MIEVVCNDRLGKGVKVCNTDGTIGDLKLLIAA 33

RESULT 3
UBL5_MESAU
ID UBL5_MESAU STANDARD; PRT; 73 AA.
AC Q6EGX7;
DT 25-OCT-2004 (Rel. 45; Created)
DT 25-OCT-2004 (Rel. 45; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Mesocricetus.
OC NCBI_TaxID=10036;
RN NUCLEOTIDE SEQUENCE.
RA Revel F., Simonneau V., Sorensen B.H., Mikkelsen J.D.;
RT "Beacon in the golden hamster.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Interacts with CLK4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY329082; AAQ99044.1; -; mRNA.
CC SMR; Q8EGX7; 1-73.
CC InterPro; IPR000626; Ubiquitin.
CC Pfam; PF00240; ubiquitin; 1.
CC DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
CC DR PROSITE; PS00053; UBIQUITIN_2; FALSE NEG.
CC KW Ubl conjugation pathway.
CC FT DOMAIN 1 73 Ubiquitin-like.
CC SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKGVKVCNTDGTIGDLKLLIAA 33
Db 1 MIEVVCNDRLGKGVKVCNTDGTIGDLKLLIAA 33

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Db 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33
? RESULT 4
ID UBL5 MOUSE STANDARD; PRT; 73 AA.
AC Q9EPV8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2005 (Rel. 45, Last sequence update)
DE Ubiquitin-like protein 5.
GN Name=UBL5;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney Pancreas, Spinal ganglion, and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Pamer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC
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CC
CC EMBL; AK002730; BAB22312.1; -; mRNA.
CC EMBL; AK003992; BAB23111.1; -; mRNA.
CC EMBL; AK007726; BAB25215.1; -; mRNA.
CC EMBL; AK009854; BAB26545.1; -; mRNA.
CC EMBL; AK012803; BAB28481.1; -; mRNA.
CC EMBL; AK051149; BAC34537.1; -; mRNA.
CC EMBL; BC028498; AAB28498.1; -; mRNA.
CC PDB; 1UH6; NMR; A=1-73.
CC MGI; MGI:1913427; Ubl5.
CC InterPro; IPR000626; Ubiquitin.
CC Pfam; PF00240; ubiquitin; 1.
CC PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
CC PROSITE; PS0053; UBIQUITIN_2; FALSE_NEG.
CC 3D-structure; Ubl conjugation pathway.
KW DOMAIN 1 73 Ubiquitin-like.
FT SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;
SQ
Query Match 99.4%; Score 163; DB 1; Length 73;
Best Local Similarity 97.0%; Pred. No. 4.5e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33
DB 1 MIEVNCNDRLGKVKVKNCTDDTIGDLKLLIAA 33
RESULT 5
UBL5 PSAOB STANDARD; PRT; 73 AA.
AC Q791B0;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2005 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Peamomys obesus (Fat sand rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Gerbillinae; Peamomys.
OX NCBI_TaxID=48139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=20527879; PubMed=11078442;
RA Collier G.R., McMillan J.S., Windmill K., Walder K., Tenne-Brown J.,
RA de Silva A., Trevisan P.J., Jones S., Morton G.J., Lee S., Augert G.,
RA Civitarese A., Zimmatt P.Z.;
RT "Beacon: a novel gene involved in the regulation of energy balance."
RL Diabetologia 49:1766-1771 (2006).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC
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CC
CC EMBL; AF318186; AAG34704.1; -; mRNA.
CC SMR; Q791B0; 1-73.
CC InterPro; IPR000626; Ubiquitin.

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DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
 DR PROSITE; PS00053; UBIQUITIN_2; FALSE_NEG.
 KW Ubl conjugation pathway.
 FT DOMAIN 1 73 Ubiquitin-like.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;
 Query Match 99.4%; Score 163; DB 1; Length 73;
 Best Local Similarity 97.0%; Pred. No. 4.5e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 RESULT 6
 QSRCIO_PONPY PRELIMINARY; PRT; 73 AA.
 ID QSRCIO7
 AC QSRCIO7
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKF2p469G145.
 GN Name=DKF2p469G145;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney.
 RG The German cDNA Consortium;
 RA Ansoerge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR858290; CAH90527.1; -; mRNA.
 DR SMR; QSRCIO; 1-73
 DR GO; GO:0006464; P;protein modification; IEA.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;
 Query Match 99.4%; Score 163; DB 2; Length 73;
 Best Local Similarity 97.0%; Pred. No. 4.5e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 RESULT 7
 Q4RSJ3_MACFA PRELIMINARY; PRT; 73 AA.
 ID Q4RSJ3
 AC Q4RSJ3
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Brain cDNA, clone: Qf1A-12296, similar to human ubiquitin-like 5 (UBL5), (Testis cDNA, clone: Qf8A-15893, similar to human ubiquitin-like 5 (UBL5)).
 DE like 5 (UBL5)).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis; and
 RT "DNA sequences of macaque genes expressed in brain or testis and its

RT evolutionary implications.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB169550; BAE01632.1; -; mRNA.
 DR EMBL; AB168933; BAE01034.1; -; mRNA.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;
 Query Match 99.4%; Score 163; DB 2; Length 73;
 Best Local Similarity 97.0%; Pred. No. 4.5e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 RESULT 8
 UBL5_BRARE STANDARD; PRT; 73 AA.
 ID UBL5_BRARE
 AC Q7SXF2;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ubiquitin-like protein 5.
 GN Name=ubl5; ORFNames=zgc:66388;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RG NIH - Zebrafish Gene Collection (ZGC) project;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC -----
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 CC -----
 DR EMBL; BC055630; AAH5630.1; -; mRNA.
 DR SMR; Q7SXF2; 1-72.
 DR ZFIN; ZDB-GENE-040426-1629; zgc:66388.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
 DR PROSITE; PS00053; UBIQUITIN_2; FALSE_NEG.
 KW Ubl conjugation pathway.
 FT DOMAIN 1 73 Ubiquitin-like.
 SQ SEQUENCE 73 AA; 8587 MW; 23716CBB0FC7C545 CRC64;
 Query Match 93.3%; Score 153; DB 1; Length 73;
 Best Local Similarity 90.9%; Pred. No. 1.1e-13;
 Matches 30; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 Db 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
 RESULT 9
 UBL5_DROME STANDARD; PRT; 73 AA.
 ID UBL5_DROME
 AC Q9V958; Q4QPS6;

DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ubiquitin-like protein 5.
 GN Name1(2)k03203; ORFNames=CG3450;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCES [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Balslev D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA LaRoche P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.W., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCES [LARGE SCALE MRNA].
 RC STRAIN=Berkley;
 RA Stapleton M., Carlson J.W., Chavez C., Frise E., George R.A.,
 RA Pacleb J.M., Park S., Wan K.H., Yu C., Celisner S.E.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.

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 CC -----
 CC EMBL: AE003790; AAF57398.1; -; Genomic DNA.
 CC EMBL: BT023690; AAY85090.1; -; mRNA.
 CC SMR: Q9V998; 1-73.
 CC Ensembl: CG3450; Drosophila melanogaster.
 CC FlyBase: FBgn0022224; 1(2)k03203.
 CC GO: GO:0005737; Cytoplasm; ISS.
 CC InterPro: IPR000826; Ubiquitin.
 CC Pfam: PF00240; ubiquitin; 1.
 CC PROSITE: PS00299; UBIQUITIN_1; FALSE_NEG.
 CC PROSITE: PS00053; UBIQUITIN_2; 1.
 KW Ubl conjugation pathway. Ubiquitin-like.
 FT DOMAIN 1 73
 SQ SEQUENCE 73 AA; 8570 MW; 0870111AC5686A70 CRC64;
 Query Match 92.7%; Score 152; DB 1; Length 73;
 Best Local Similarity 87.9%; Pred. No. 1.6e-13;
 Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MIEVNCNRLGKGVKVCNTDTTIGDLKLLIAA 33
 DB 1 MIEITCNRLGKGVKVCNPDITIGDLKLLIAA 33
 RESULT 10
 QSHZC1 XENLA PRELIMINARY; PRT; 73 AA.
 AC QSHZC1;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marulima K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089084; AAH89084.1; -; mRNA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8635 MW; 2A51E123F36FF390 CRC64;

Query Match 92.1%; Score 151; DB 2; Length 73;
Best Local Similarity 90.9%; Pred. No. 2.2e-13;
Matches 30; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 11
Q7QHM2 ANOQA PRELIMINARY; PRT; 73 AA.
AC Q7QHM2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANGP0000015674
GN ORFNames=ENSANGG00000013185;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008816; EAA05206.2; -; Genomic_DNA.
DR SMR; Q7QHM2; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8599 MW; 43D212BE601B3C0D CRC64;

Query Match 91.5%; Score 150; DB 2; Length 73;
Best Local Similarity 84.8%; Pred. No. 3e-13;
Matches 28; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 12
Q4SMI6 TETNG PRELIMINARY; PRT; 73 AA.
ID Q4SMI6_TETNG

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AC Q4SMI6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 18 SCAP14547, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00015743001;
GN Tetraodon nigroviridis (Green puffer);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Nuclei S., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Maucell E., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014547; CAF98146.1; -; Genomic_DNA.
FT NON TER 73
SQ SEQUENCE 73 AA; 8592 MW; 6A14CA0323F8E8EB CRC64;

Query Match 89.6%; Score 147; DB 2; Length 73;
Best Local Similarity 87.9%; Pred. No. 8e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 13
UBLS_ARATH
ID UBLS_ARATH STANDARD; PRT; 73 AA.
AC Q9FGZ9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=UBLS; OrderedLocustNames=At5g42300; ORFNames=K5J14.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";

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DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8529 MW; -FDA1CGED0770F525 CRC64;

Query Match 89.0%; Score 146; DB 2; Length 73;
Best Local Similarity 87.9%; Pred.No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0

QY 1 MIEVWCNDRLGKKVKVCNTDDTIGDLKKLIAA 33
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MIEVWLNDRLGKKVKVCNDDTIGDLKKLVAA 33

RESULT 15
Q570V8 ARATH PRELIMINARY; PRT; 73 AA.
ID AC Q570V8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Ubiquitin-like protein.
GN Name=At5g42300;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK220599; BAD94931.1; -; mRNA.
SQ SEQUENCE 73 AA; 8571 MW; 4F20CGED077133F6 CRC64;

Query Match 89.0%; Score 146; DB 2; Length 73;
Best Local Similarity 87.9%; Pred.No. 1.1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 0; Gaps 0

QY 1 MIEVWCNDRLGKKVKVCNTDDTIGDLKKLIAA 33
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MIEVWLNDRLGKKVKVCNDDTIGDLKKLVAA 33

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Job time : 232 secs

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